BIOTECHNOLOGY
SYSTEMS
BRANCH

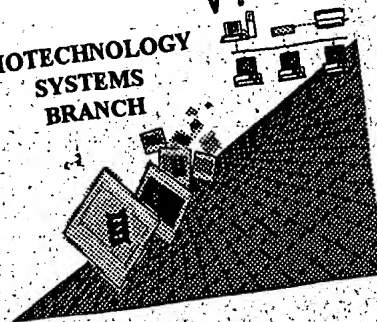# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/901,001·A_

Source: _OIPE_

Date Processed by STIC: _7/6/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

```
┌─────────────────────────────────────────────────────┐
│   This Raw Listing contains the General              │
│   Information Section and those Sequences            │
│   containing ERRORS.                                 │
└─────────────────────────────────────────────────────┘
```

Does Not Comply
Corrected Diskette Needed

```
     1    <110> ASAHIKASEI KOGYO KABUSHIKI KAISHA
     2          ASAHI MEDICAL CO., LTD.
     3    <120> Separating apparatus of cells and separating method
     4    <130> ASAHI-1
     5    <150> JP 10/159957
     6    <151> 1998-5-25
     7    <160> 48
```

ERRORED SEQUENCES FOLLOW

```
        8     <210> 41
E-->    9     <211> (879) 909 (p.2)
        10    <212> DNA
        11    <213> mouse
        12    <400> 41
```

*use lower-case letters for
bases when Sequence Listing is
in new Sequence Rules format*

```
W-->   13        atg acc atg att acg cca agc ttt gga gcc ttt ttt ttg gag att ttc 48
       14        Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe
       15                             5               10              15
W-->   16        aac gtg aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc tat 96
       17        Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr
       18                         20              25              30
W-->   19        gcg gcc cag ccg gcc atg gcc cag gtg aag ctg cag cag tct gga cct144
       20        Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Gln Ser Gly Pro
       21                         35              40              45
W-->   22        ggc cta gtg cag ccc tca cag agc ctg tcc ttc atc tgc aca gtc tct    192
       23        Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Phe Ile Cys Thr Val Ser
       24                         50              55              60
W-->   25        ggt ttc tca tta act agt cat ggt gta cac tgg gtt cgc cag tct cca    240
       26        Gly Phe Ser Leu Thr Ser His Gly Val His Trp Val Arg Gln Ser Pro
       27             65              70              75              80
W-->   28        gga aag ggt ctg gag tgg ctg gga gtg ata tgg ggt gct gga agg aca    288
       29        Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ala Gly Arg Thr
       30                         85              90              95
W-->   31        gac tat aat gca gct ttc ata tcc aga ctg agc atc agc agg gac att    336
       32        Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Ser Arg Asp Ile
       33                         100             105             110
W-->   34        tcc aag agc caa gtt ttc ttt aag atg aac agt ctg caa gtt gat gac    384
       35        Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Val Asp Asp
       36                         115             120             125
W-->   37        aca gcc ata tat tac tgt gcc aga aat agg tac gag agc tac ttt gac    432
       38        Thr Ala Ile Tyr Tyr Cys Ala Arg Asn Arg Tyr Glu Ser Tyr Phe Asp
       39                         130             135             140
```

OIPE

```
W-->   40        tac tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc ggt    480
       41        Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
       42        145                 150                 155                 160

W-->   43        tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac atc gag ctc act    528
       44        Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
       45                            165                 170                 175

W-->   46        cag tct cca ctc tcc ctg cct gtc agt ctt gga gat cag gcc tcc atc    576
       47        Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile
       48                            180                 185                 190

W-->   49        tct tgc aga tct agt cag aac ctt gta cac agt aat gga aat acc tat    624
       50        Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser Asn Gly Asn Thr Tyr
       51                            195                 200                 205

W-->   52        tta cat tgg tac ctg cag aag cca ggc cag tct cca aat ctc ctg atc    672
       53        Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu Leu Ile
       54                            210                 215                 220

W-->   55        tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc    720
       56        Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
       57        225                 230                 235                 240

W-->   58        agt gga tca ggg aca gaa ttc aca ctc aag atc agc aga gtg gag gct    768
       59        Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
       60                            245                 250                 255

W-->   61        gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg ctc    816
       62        Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu
       63                            260                 265                 270

W-->   64        acg ttc ggt gct ggg acc aag gtg gag ctg aaa cgg gcg gcc gca ggt    864
       65        Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Gly
       66                            275                 280                 285

W-->   67        gcg ccg gtg ccg tat ccg gat ccg ctg gaa ccg cgt gcc gca tag    909
       68        Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg Ala Ala
       69                            290                 295                 300
```

```
       70   <210> 45
       71   <211> 9
       72   <212> PRT
       73   <213> Artificial Sequence
       74   <220>
       75   <223> Amino acid sequence of heavy chain CDR-3
       76   <400> 45
       77        Asn Arg Tyr Glu Ser Tyr Phe Asp Tyr
                 1                 5
```

← number the amino acids under every 5 amino acids.

```
       78   <210> 47
       79   <211> 13
       80   <212> PRT
       81   <213> Artificial Sequence
       82   <220>
       83   <223> Amino acid sequence of light chain CDR-2
       84   <400> 47
       85        Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
                 1                 5                 10
```

DO NOT use TAB codes between amino acid nos.

The above errors are samples of global errors. Please ensure all amino acids are properly numbered.

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/701,001A**

Input Set: **I701001A.RAW**

Line	?	Error/Warning	Original Text
9	E	Input 879, Calc# Bases 909 differ	<211> 879
13	W	Line data has been corrected	ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC T
16	W	Line data has been corrected	AAC GTG AAA AAA TTA TTA TTC GCA ATT CCT T
19	W	Line data has been corrected	GCG GCC CAG CCG GCC ATG GCC CAG GTG AAG C
22	W	Line data has been corrected	GGC CTA GTG CAG CCC TCA CAG AGC CTG TCC T
25	W	Line data has been corrected	GGT TTC TCA TTA ACT AGT CAT GGT GTA CAC T
28	W	Line data has been corrected	GGA AAG GGT CTG GAG TGG CTG GGA GTG ATA T
31	W	Line data has been corrected	GAC TAT AAT GCA GCT TTC ATA TCC AGA CTG A
34	W	Line data has been corrected	TCC AAG AGC CAA GTT TTC TTT AAG ATG AAC A
37	W	Line data has been corrected	ACA GCC ATA TAT TAC TGT GCC AGA AAT AGG T
40	W	Line data has been corrected	TAC TGG GGC CAA GGG ACC ACG GTC ACC GTC T
43	W	Line data has been corrected	TCA GGC GGA GGT GGC TCT GGC GGT GGC GGA T
46	W	Line data has been corrected	CAG TCT CCA CTC TCC CTG CCT GTC AGT CTT G
49	W	Line data has been corrected	TCT TGC AGA TCT AGT CAG AAC CTT GTA CAC A
52	W	Line data has been corrected	TTA CAT TGG TAC CTG CAG AAG CCA GGC CAG T
55	W	Line data has been corrected	TAC AAA GTT TCC AAC CGA TTT TCT GGG GTC C
58	W	Line data has been corrected	AGT GGA TCA GGG ACA GAA TTC ACA CTC AAG A
61	W	Line data has been corrected	GAG GAT CTG GGA GTT TAT TTC TGC TCT CAA A
64	W	Line data has been corrected	ACG TTC GGT GCT GGG ACC AAG GTG GAG CTG A
67	W	Line data has been corrected	GCG CCG GTG CCG TAT CCG GAT CCG CTG GAA C

CORRECTION SUMMARY
PATENT APPLICATION **US/09/701,001A**

Input Set: **I701001A.RAW**

Line	Original Text	Corrected Data
13	ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC T	atg acc atg att acg cca agc ttt gga gcc t
16	AAC GTG AAA AAA TTA TTA TTC GCA ATT CCT T	aac gtg aaa aaa tta tta ttc gca att cct t
19	GCG GCC CAG CCG GCC ATG GCC CAG GTG AAG C	gcg gcc cag ccg gcc atg gcc cag gtg aag c
22	GGC CTA GTG CAG CCC TCA CAG AGC CTG TCC T	ggc cta gtg cag ccc tca cag agc ctg tcc t
25	GGT TTC TCA TTA ACT AGT CAT GGT GTA CAC T	ggt ttc tca tta act agt cat ggt gta cac t
28	GGA AAG GGT CTG GAG TGG CTG GGA GTG ATA T	gga aag ggt ctg gag tgg ctg gga gtg ata t
31	GAC TAT AAT GCA GCT TTC ATA TCC AGA CTG A	gac tat aat gca gct ttc ata tcc aga ctg a
34	TCC AAG AGC CAA GTT TTC TTT AAG ATG AAC A	tcc aag agc caa gtt ttc ttt aag atg aac a
37	ACA GCC ATA TAT TAC TGT GCC AGA AAT AGG T	aca gcc ata tat tac tgt gcc aga aat agg t
40	TAC TGG GGC CAA GGG ACC ACG GTC ACC GTC T	tac tgg ggc caa ggg acc acg gtc acc gtc t
43	TCA GGC GGA GGT GGC TCT GGC GGT GGC GGA T	tca ggc gga ggt ggc tct ggc ggt ggc gga t
46	CAG TCT CCA CTC TCC CTG CCT GTC AGT CTT G	cag tct cca ctc tcc ctg cct gtc agt ctt g
49	TCT TGC AGA TCT AGT CAG AAC CTT GTA CAC A	tct tgc aga tct agt cag aac ctt gta cac a
52	TTA CAT TGG TAC CTG CAG AAG CCA GGC CAG T	tta cat tgg tac ctg cag aag cca ggc cag t
55	TAC AAA GTT TCC AAC CGA TTT TCT GGG GTC C	tac aaa gtt tcc aac cga ttt tct ggg gtc c
58	AGT GGA TCA GGG ACA GAA TTC ACA CTC AAG A	agt gga tca ggg aca gaa ttc aca ctc aag a
61	GAG GAT CTG GGA GTT TAT TTC TGC TCT CAA A	gag gat ctg gga gtt tat ttc tgc tct caa a
64	ACG TTC GGT GCT GGG ACC AAG GTG GAG CTG A	acg ttc ggt gct ggg acc aag gtg gag ctg a
67	GCG CCG GTG CCG TAT CCG GAT CCG CTG GAA C	gcg ccg gtg ccg tat ccg gat ccg ctg gaa c